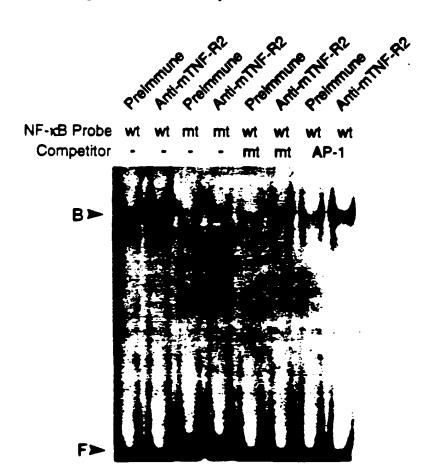
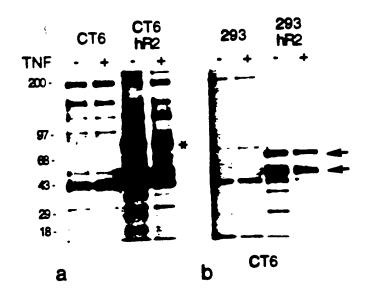
# Activation of the Transcription Factor NF-κB through TNF Receptor 2 in CT6 Cells







### Immunoprecipitation of Human TNF Receptor 2



Glutathione-S-Transferase human TNF Receptor 2 Intracellular Domain Fusion Protein

1

#### Coprecipitation of Glutathione-S-Transferase Human TNF Receptor 2 Intracellular Domain Fusion Protein in CT6 Cell Extracts







# Coprecipitation of Glutathione-S-Transferase Mutant Human TNF Receptor 2 Intracellular Domain Fusion Proteins in CT6 Cell Extracts

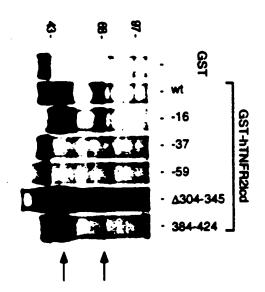
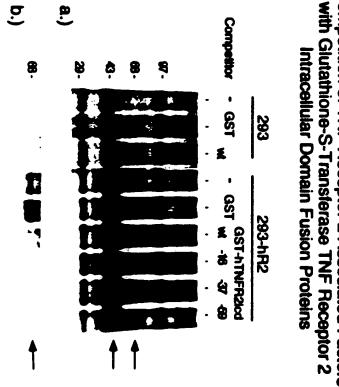


Figure 5

516/911/80



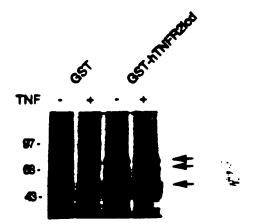




**CT6** 

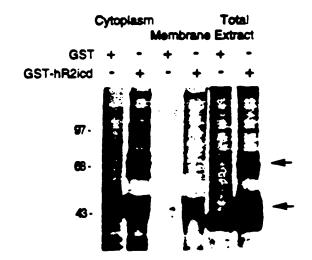
4

#### Coprecipitation of Glutathione-S-Transferase Human TNF Receptor 2 Intracellular Domain Fusion Protein in Jurkat Cell Extracts



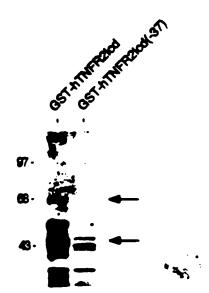


## Intracellular Localization of TNF Receptor 2 Associated Factors





## Purification of TNF Receptor 2 Associated Factors







- CCCAGCCGGTTCTCTGCCCCAAGGACGCTACCGCCCAATOCGAGCAGAAGGCGGCGCACAGATACAGAAAGT 74 GAGGCTCAGACATATTGAAGACCGTGTGACATAGGGTAGCCAAATGACAGTGTGAGAAAGTGACATTTACTCAAG 149 GCCACCCAGATATCCTGGAGGACCCAGAACCCTGGAGATTCCCATCAGAAAGACCTTCTGGCCACCTGAAACCCC MetAlaSerSerSerAlaProAspGluAsnGluPheGlnPheGlyCysProProAlaProCysGlnAspPro 224 AASATGGCCTCCAGCTCAGCCCCTGATGAAAACGAGTTTCAATTTGGTTGCCCCCCCTGCTCCCTGCCAGGACCCA 25 SerGluProArgValLeuCysCysThrAlaCysLeuSerGluAsnLeuArgAspAspGluAspArgIleCysPro 299 TCGGAGCCCAGAGTTCTCTOCTOCACAGCCTGTCTCTCTGAGAACCTGAGAGGATGAGGATCAGGATCTGTCCT 50 LysCysArgAlaAspAsnLeuHisProValSerProGlySerProLeuThrGlnGluLysValHisSerAspVal 374 AAATGCAGAGCAGACAACCTCCATCCTOTGAGCCCAGGAAGCCTCTGACTCAGGAGAAGGTTCACTCTGATGTA 75 AlaGluAlaGluIleMetCysProPheAlaGlyValGlyCysSerPheLysGlySerProGlnSerMetGlnGlu 449 GCTGAGGCTGAAATCATGTGCCCCTTTGCAGGTGTTGGCTGTTCCTTCAAGGGGAGCCCACAATCCATGCAGGAG 100 HisGluAlaThrSerGlnSerSerHisLeuTyrLeuLeuAlaValLeuLysGluTrpLysSerSerFroGly 524 CATGAGGCTACCTCCCAGTCCTCCCACCTGTACCTGCTGCCGGGTCTTAAAGGAGTGGAAATCCTCACCAGGC 125 SerksnieuglySerklaProMethlaLouglukrgksnieuSergluLouglnieuglnklaAlaValglukla 599 TCCAACCTAGGGTCTGCACCCATGGCACTGGAGCGGAACCTGTCAGAGCTGCAGCTTCAGGCAGCTGTGGAAGCG 150 ThrGlyAspLeuGluValAspCysTyrArgAlaProCysCysGluSerGlnGluGuLeuAlaLeuGlnHisLeu 674 ACAGGGGACCTGGAGGTAGACTGCTACCGGGCACCTTGCTGTAGAGCCCAGGAAGAACTGGCCCTGCAGCACTTG 175 VallysGluLysLeuLeuAlaGlnLeuGluGluLysLeuArgValPheAlaAsnIleValAlaValLeuAsnLys 749 GTGAAGGAGAAGCTGCTGGCTCAGCTGGAGGAGAAGCTGCGTGTGTTTGCAAACATTGTTGCTGTCCTCAACAAG 200 GluValGluAlaSerHisLeuAlaLeuAlaAleSerIlaHisGlnSerGlnLeuAspArgGluHisLeuLeuSer 215 LeuGluGlnArgValValGluLeuGlnGlnThrLeuAlaGlnLysAspGlnValLeuGlyLysLeuGluHisSer ESS TTGGAGCAGGGGGGGGGGAATTACAGCAAACCCTGGCTCAAAAAGACCAGGTCCTGGGCAAGCTTGAGCACAGT 251 LeuArgLeuMetGluGluAlaSerPheAspGlyThrPheLeuTrpLysIleThrAsnValThrLysArgCysHis 914 CTSCGACTCATGGAGGAGGCATCCTTTGATGGTACTTTCCTGTGGAAGATCACCAATGTCACCAAGCGGTGCCAC 275 GluSerValCysGlyArgThrValSerLeuPheSerProAlaPheTyrThrAlaLysTyrGlyTyrLysLeuCys 1149 GASTEASTGTGTGGCCGGACTGTCAGCCTCTTCTCCCAGCTTTCTACACTGCCAAGTATGGTTACAAGTTGTGC 300 LeuhrgLeuTyrLeuhsnGlyhspGlySerGlyLysLysThrHisLeuSerLeuPheIleValIleMetArgGly 1124 CTGCGCTTGTACCTGAACGGGGATGGCTCAGGCAAGAAGACCCACCTGTCCCTCTTCATCGTGATCATGAGAGGA 315 GluTyrAspAlaLeuLeuProTrpProPheArgAsnLysValThrPheMetLeuLeuAspGlnAsnAsnArgGlu 1199 GAATACGATGCTCTCCTGCCCTGGCCTTTCAGGAACAAGGTCACCTTTATGCTACTTGACCAGAACAACCGAGAG 351 HisalalleAspalaPheArgProAspLeuSerSerAlaSerPheGlnArgProGlnSerGluThrAsnValala 1274 CATGOTATTGATGCCTTCCGGCCTGACCTGAGCTCAGCCTCCTTCCAGCGGCCACAGAGTGAGACCAACGTGGCC 375 SerGlyCysProLeuPhePheProLeuSerLysLeuGlnSerProLeuSiallaTyzValLyslaphapThrMet 1349 ASSESSTED COCCOCTCTCTTCCCCCTCAGCAAGCTGCAGTCACCCCAAGCACGCCTACGTCAAGATGACACAATG 400 PhoLoulysCysIleValAspThrSerAla 1499 TGGGGGACTTAGCTAGACAGCCAGGCCCTGCCTTGCCCTTTGGAGCCCACGACCACGACAAGCAGGCCAAGGCT 1574 GGCATGACTTCAGCGCCACAGCATGCTGGTTATGGCTGATGTGAGGCTGGAGAAACGTGTGCGTACAGAGACAGA 1649 GTGGAGGAGAAGACAGAAGTGCTCTTTTCACACAGACTACACGACACCAGGAGGCCAGCATGCCAGCAGCTTCTG 1724 AATGTTGAGACCAGCCTAGATCAGGATGAAAAGAGCCAGGCCTGAGGCTTGGACATTGAGCCAAGGCTATGGGGC

1799 CTAAGTGGAGGGGCACTCCTACCAGGACATTCTCTGAGGTCAGGGCATAACTGGAAAAATGCCCCCATCTCTCT 1874 GTTCAGACTCAAAACTAGAACCACAGGGCAGAAGGGTCAGACATTAATGTGAATTTAACCTGCCCTGGACTGAGT 1949 TCCTATGTTAACAGACACGCAAACAGGTAAACCCAGAAACTGCCCTGGGAAATGCTTTCTGGCTGCATCTGGAGA





MethlahlahlaSerValThrSerPro GCGCGAAGACCGTTGGGGCTTTGTGGTGTGTGGGGGTTGTAACTCACATGGCTGCAGCCAGTGTGACTTCCCCT 10 GlySerLeuGluLeuLeuGlnProGlyPheSerLysThrLeuLeuGlyThrArgLeuGluAlaLysTyrLeuCys 75 GGCTCCCTAGAACTGCTACAGCCTGGCTTCTCCAAGACCCTCCTGGGGACCAGGTTAGAAGCCAAGTACCTCTGT 35 SerAlaCysLysAsnIleLeuArgArgProPheGlnAlaGlnCysGlyEisArgTyTCysSerPheCysLeuThr 150 TCAGCCTGCAAAAACATCCTGCGGAGGCCTTTCCAGGCCCAGTGTGGGCACCGCTACTGCTCCTTCTGCCTGACC 60 SerileLeuSerSerGlyProGlnAsnCyeAlaAlaCyeValTyrGluGlyLeuTyrGluGluGlyIleSerIle 225 AGCATCCTCAGCTCTGGGCCCCAGAACTGTGCTGCCTGTGTCTATGAAGGCCTGTATGAAGAAGGCATTTCTATT 85 LeuGluSerSerSerAlaPheProAspAsnAlaAlaArgArgGluValGluSerLeuProAlaValCysProAsn 300 TTAGAGAGTAGTTCGGCCTTTCCAGATAACGCTGCCCGCAGAGAGGGGGGAGAGCCTGCCAGCTGTCTCTCCCAAT 110 AspGlyCysThrTrpLysGlyThrLeuLysGluTyrGluSerCysHisGluGlyLeuCysProPheLeuLeuThr 375 GATGGATGCACTTGGAAGGGGACCTTGAAAGAATACGAGACTGCCACGAAGGACTTTGCCCATTCCTGCTGACG 135 GluCysProAlaCysLysGlyLeuValArgLeuSerGluLysGluHisHisThrGluGlnGluCysProLysArg 450 GAGTGTCCTGCATGTAAAGGCCTGGTCCGCCTCAGCGAGAAGGAGCACCACACTGAGCAGGAATGCCCCAAAAGG 160 SerLeuSerCvsGlnHisCvsArgAlaProCysSerHisValAspLeuGluValHisTyrGluValCvsProLys 525 AGCCTGAGCTGCCAGCACTGCAGAGCACCCTGTAGCCACGTGGACCTGGAGGTACACTATGAGGTCTGCCCCAAG 185 PheProLeuThrCysAspGlyCysGlyLysLysLysIleProArgGluThrPheGlnAspHisValArgAlaCys 600 TTTCCCTTAACCTGTGATGGCTGTGGCAAGAAGAAGATCCCTCGGGAGACGTTTCAGGACCATGTTAGAGCATGC 210 SerLysCysArgValLeuCysArgPheHisThrValGlyCysSerGluMetValGluThrGluAsnLeuGlnAsp 675 AGCAAATGCCGGGTTCTCTGCAGATTCCACACCGTTGGCTGTTCAGAGATGGTGGAGACTGAGAACCTGCAGGAT 235 HisGluLeuGlnArgLeuArgGluHisLeuAlaLeuLeuLeuSerSerPheLeuGluAlaGlnAlaSerProGly 751 CATGAGCTGCAGCGGCTACGGGAACACCTAGCCCTACTGCTGAGCTCATTCTTGGAGGCCCAAGCCTCTCCAGGA 261 ThrieuAsnGlnValGlyProGluLeuLeuGlnArgCysGlnIleLeuGluGlnLysIleAlaThrPheGluAsn E25 ACCTTGAACCAGGTGGGGCCAGAGCTACTCCAGCGGTGCCAGATTTTGGAGCAGATAGCAACCTTTGAGAAC 285 IleValCysValLeuAsnArgGluValGluArgValAlaValThrAlaGluAlaCysSerArgGlnHisArgLeu 911 ATTGTCTGCGTCTTGAACCGTGAAGTAGAGAGGGTAGCAGTGACTGCAGAGGCTTGTAGCCGGCAGCACCGGCTA 310 Asp@lnAsplysIleGluAlaLeuSerAsnLysValGinGlnLeuGluArgSerIleGlyLeuLysAspLeuAla 975 GACCAGGACAAGATTGAGGCCCTGAGTAACAAGGTGCAACAGCTGGAGAGGAGCATCGGCCTCAAGGACCTGGCC 335 MethlakspLeuGluGlnLysValSerGluLeuGluValSerThrTyrAspGlyValPheIleTrpLysIleSer 1050 ATGGCTGACCTGGAGCAGAAGGTCTCCGAGTTGGAAGTATCCACCTATGATGGGGTCTTCATCTGGAAGATCTCT 360 AspPheThrArgLysArgGlnGluAlaValAlaGlyArgThrProAlaIlePheSerProAlaPheTyrThrSer 1125 GACTTCACCAGAAAGCGTCAGGAAGCCGTAGCTGGCCGGACACCAGCTATCTTCTCCCCAGCCTTCTACACAAGC 385 ArgTyrGlyTyrLysMetCysLeuArgValTyrLeuAsnGlyAspGlyThrGlyArgGlyThrHisLeuSerLeu 12:1 ASATATGGCTACAAGATGTGTCTACGAGTCTACTTGAATGGCGACGGCACTGGGCGGGGAACTCATCTGTCTCTC 410 PhePheValValMetLysGlyProAsnAspAlaLeuLeuGlnTrpProPheAsnGlnLysValThrLeuMetLeu 1275 TTCTTCGTGGTGATGAAAGGCCCCAATGATGCTCTGTTGCAGTGGCCTTTTAATCAGAAGGTAACATTGATGTTG 435 LeuAspHisAsnAsnArgGluHisValIleAspAlaPheArgProAspValThrSerSerSerPheGlnArgPro 135: CTGGACCATAACAACCGGGAGCATGTGATCGACGCATTCAGGCCCGATGTAACCTCGTCCTCCAGAGGCCT 461 ValSerAspMetAsnIleAlaSerGlyCysProLeuPheCysProValSerLysMetGluAlaLysAsnSerTyr 1425 GTCAGTGACATGAACATCGCCAGTGGCTGCCCCCTCTTCTGCCCTGTGTCCAAGATGGAGGCCAAGAATTCCTAT 485 ValArgAspAspAlaIlePheIleLysAlaIleValAspLeuThrGlyLeu 1500 GTGCGGGATGATGCGATCTTCATCAAAGCTATTGTGGACCTAACAGGACTCTAGCCACCCCTGCTAAGAATAGCA 1575 GCTCAGTGAGGAGCTGTCACATTAGGCCAGCCAGGCCTGCCACACACGCGTGGGCAGGCTTGGTGTAAATGCTG 1650 GGSAGGGCCTCAGCCTAGAGCCAATCACCATCACACAGAAAGGCAGGAAGAAGCCTCCAGTTGGCCTTCAGCTGG 1725 CAAACTGAGTTGGACGGTCCACTGAGCTCAAGGGCCTGGTGGAGCCCGCTGGGGAGCTTCTCAGCTTTCCAATAG 1951 TACACAGGAGAAGGCATGCGCCTGCAGGGTGTAGCCCCAAGAGAGAAGCTCTCTGAGACATAGGCCCTCACTGGAG 2025 AAGGGCTGCCTGGGCTGCACAGCCTTGCCAGGTGGCCTGTATGGGGGAGAAGTGATTAAATGTTGAGATGTCAC 2100 ACGACAAAAAAAAAAAAAAAA

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V	

consensus	c-cbl (human)	RFP (human)	RPT-1 (mouse)	RING1 (human)	SS-A/Ro (human)	RAG-1 (human)	UVS-2 (N. crassa)	RAD-18 (S. cer	EFP (human)	COP1 (A. thaliana)	TRAF2 (mouse)
							158 <b>4</b> )	(S. cerevisiae)		liana)	
	378	13	12	16	13	290	31	25	10	49	31
X11-12 X:	FQLCKICAENDKDVKIE PCGHLMCTSCLTS WQESEGQ GSSGCPFCRCE	ETTCPVCLQYFAEPHML DCGHNICCACLARCWGTA	EVTCPICLELLKEPVSA DCNHSFCRACITLNYESNRNTDGKGNCPVCRVP	ELACPICLDMLKNTWTTKECLHRPCSDCIVTA	EVTCPICLDPFVEPVSI BCGHSFCQECISQV	SISCQICEHILADPVET NCKHVFCRVCILRC	AFRCHVCKDFYDSPHLT SCNHTFCSLCIRRC	LLRCHICKDFLKVPVLT PCGHTPCSLCIRTH	ELSCSICLEPFKEPVTT PCGHNFCGSCLNETWA VQG	DLLCPICHQIIKDAFLT ACGHSFCYHCIITH	KYLCSACKNILRRPFQA QCGHRYCSFCLTSI
X10-16	<b>D</b> SES		SNRNT	LRS	GKG	NY1	LSV DSK	EN	VQG	LRN	SST
CC	GSSGCPFCRCE	ETNVSCPQCRET	DGKGNCPVCRVP	GNKE <b>CPTC</b> RKK	GGSVCAVCRQR	MGSYCPSCRYP	DSK CPLCRAT	QPNCPLCLPE	SPYLCPQCRAV	KSDCPcCSQH	GPQNCAACVYE

Pigure 12a

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OS	PDDGLVACPICLTRM KEOOVDRHLDTSC	182	(N. crassa)	Ŝ.	UVS-2	
Ö	PNEQMAQCPICQQFYPLKALEKT <b>H</b> LD	183	(S. cerevisiae)	(S.	RAD18	
HI	SEEKPFECEECGKKFRTARHLVKHQR IH	293	(mouse)	ao	MFG2	
HV	RKKPPHICGECGKGFRHPSALKKHIR VH	521	(mouse)	(m)	ZFY1/2	
HT	TGEKPYTCTVCGKKFIDRSSVVKHSR TH	1225	(X. laevis)	?	XPIN	
HV	TGKYPFICSECGKSFMDKRYLKIHSN VH	-	(X. laevis)	æ.	XLCOF14	
H	QD LAVCDVCNRKFRHKDYLRD <b>H</b> QK	189	(X. laevis)	?	TFIIIA	
ð	GGPKLVT <b>C</b> DF <b>C</b> KRDDIKKKELET <b>H</b> YK	171	(D. discoideum)	D.	DG17	
Š	pkfplt <b>C</b> dG <b>C</b> GkkkIpretfQd <b>H</b> vr	182				
గ్	CPKRSLSCQHC RAPCSHVDLEV <b>H</b> YE VC	157	(mouse)	(mo	TRAF2	

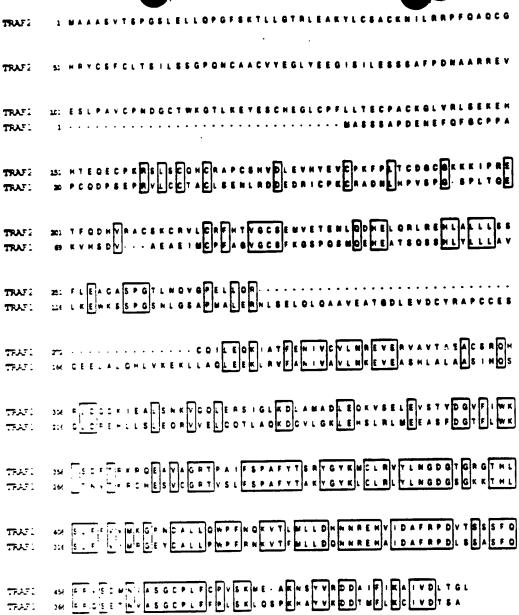


Figure 13

. Wed May 11 18:23:38 1994 ?/home/oz/vo/Molbio/rothe/p1.TRAF1 (length: 409) kyte (hydropathy); window: 20

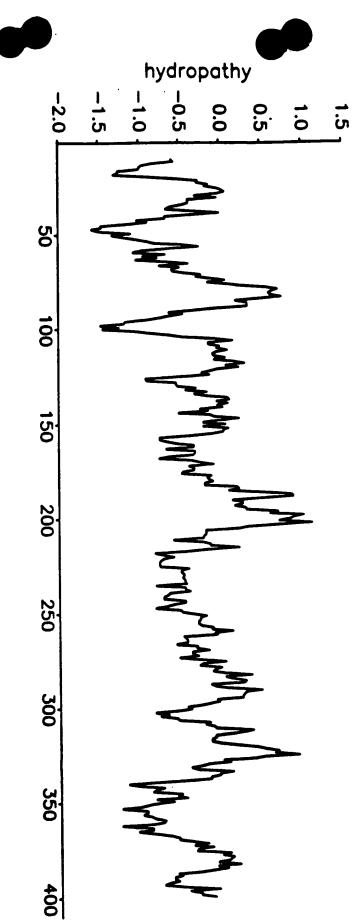


Figure 14a

wed May 1) 18:23:52 1994
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kyte (hydropathy); window: 20

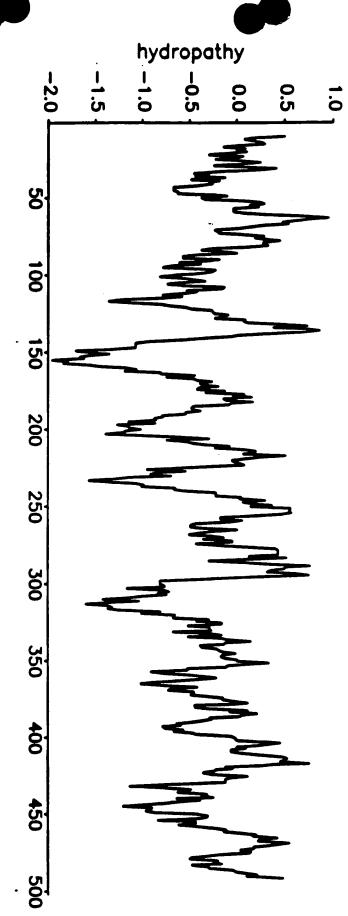


Figure 14b

TRAF Expression in CT6 Cells

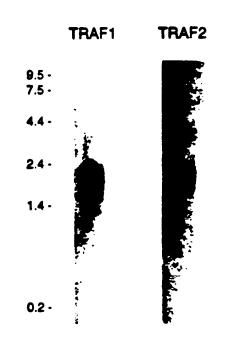
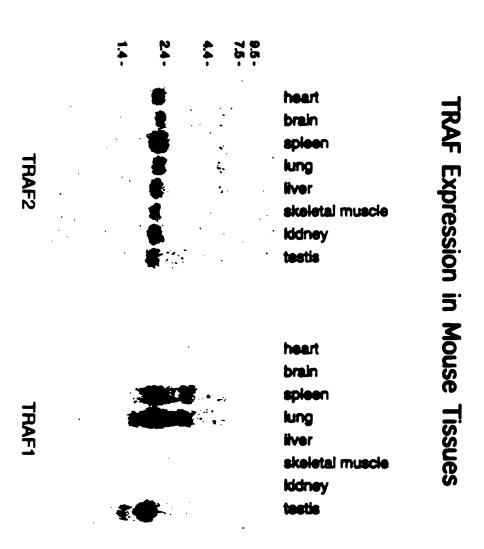


Figure 15a

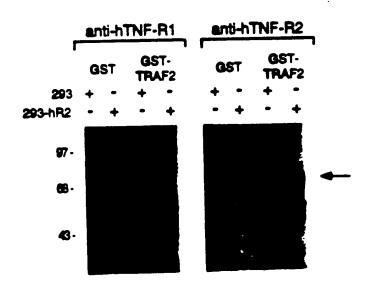


Figure 15b



T

## A Glutathione-S-Transferase TRAF2 Fusion Protein Coprecipitates the Human TNF-R2 in 293 Cell Extracts







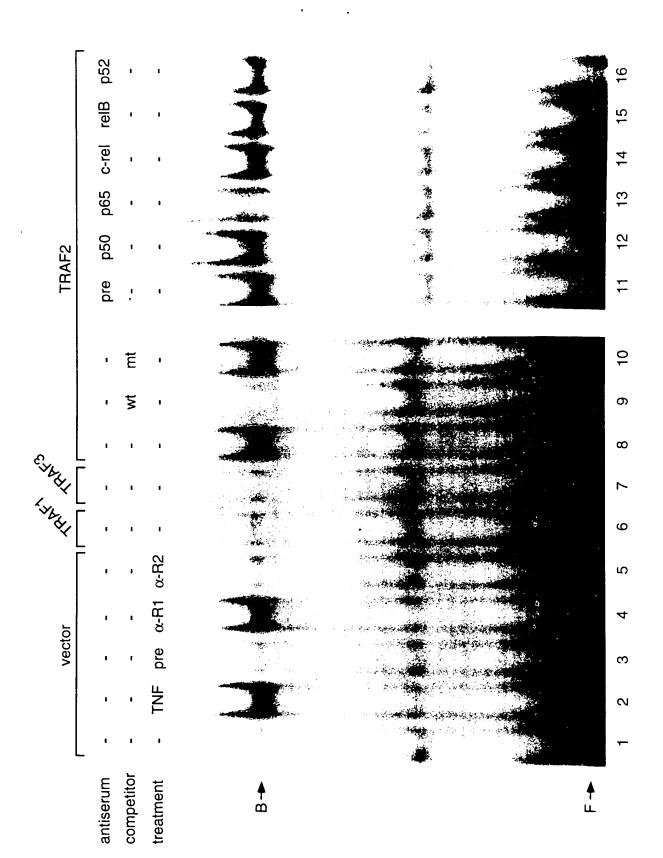
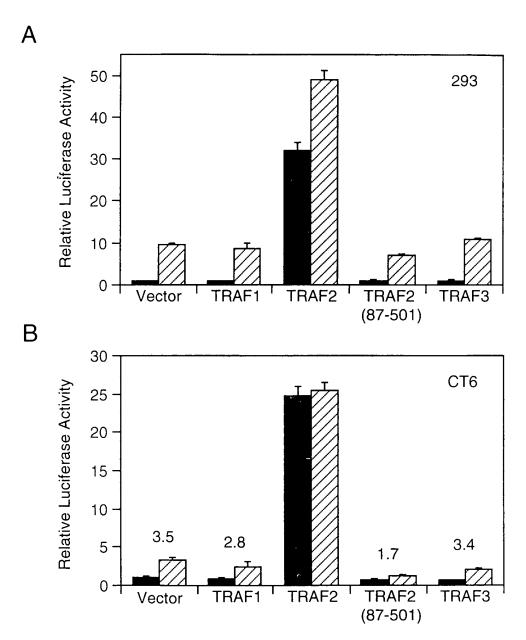






Figure 18

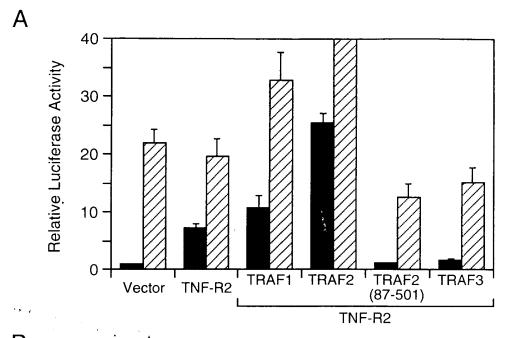


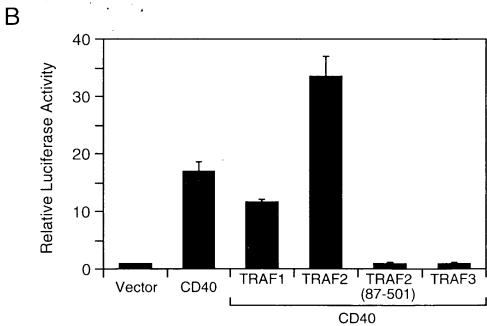
Transfected DNA





Figure 19





Transfected DNA